

SEQUENCE LISTING

<110> Ajinomoto Co., Inc.

<120> A method of secreting and producing proteins

<130> Y1J0182

<140>

<141>

<150> JP 2001-98808

<151> 2001-03-30

<160> 60

<170> PatentIn Ver. 2.1

<210> 1

<211> 43

<212> PRT

<213> Corynebacterium glutamicum

<400> 1

Met Arg Asp Thr Ala Phe Arg Ser Ile Lys Ala Lys Ala Gln Ala Lys
1 5 10 15

Arg Arg Ser Leu Trp Ile Ala Ala Gly Ala Val Pro Thr Ala Ile Ala
20 25 30

Leu Thr Met Ser Leu Ala Pro Met Ala Ser Ala
35 40

<210> 2

<211> 30

<212> PRT

<213> Corynebacterium glutamicum

<400> 2

Met Phe Asn Asn Arg Ile Arg Thr Ala Ala Leu Ala Gly Ala Ile Ala
1 5 10 15

Ile Ser Thr Ala Ala Ser Gly Val Ala Ile Pro Ala Phe Ala
20 25 30

<210> 3

<211> 25

<212> PRT

<213> Corynebacterium ammoniagenes

<400> 3

Met Lys Arg Met Lys Ser Leu Ala Ala Ala Leu Thr Val Ala Gly Ala
1 5 10 15

Met Leu Ala Ala Pro Val Ala Thr Ala

<210> 4
 <211> 782
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (579)..(782)

<400> 4
 aaattcctgt gaatttagctg atttagtact tttcggaggt gtctattctt accaaatcgt 60
 caagttgtgg gtagagtcac ctgaatatta attgcaccgc acgggtgata tatgcttatt 120
 tgctcaagta gttcgagggtt aagtgtattt taggtgaaca aatttcagct tcgggtagaa 180
 gactttcgat gcgcttcaga gcttcttattt ggaaatctga caccacttga taaaatagcc 240
 tacccccgaat ttgggggatt ggtcatttt tgctgtgaag gtagtttga tgcatatgac 300
 ctgcgtttat aaagaaatgt aaacgtgatc agatcgatat aaaagaaaca gtttgtactc 360
 aggttgaag cattttctcc gattcgcctg gcaaaaatctt caattgtcgc ttacagtttt 420
 tctcaacgac aggctgctaa gctgctagtt cggtgcccta gtgagtggcg tttacttgg 480
 taaaagtaat cccatgtcgt gatcagccat tttgggttgt ttccatagca atccaaaggt 540
 ttctgttttc gataccattt caaggagcc tcgcctct atg ttt aac aac cgt atc 596
 Met Phe Asn Asn Arg Ile
 1 5

cgc act gca gct ctc gct ggt gca atc gca atc tcc acc gca gct tcc 644
 Arg Thr Ala Ala Leu Ala Gly Ala Ile Ala Ile Ser Thr Ala Ala Ser
 10 15 20

ggc gta gct atc cca gca ttc gct cag gag acc aac cca acc ttc aac 692
 Gly Val Ala Ile Pro Ala Phe Ala Gln Glu Thr Asn Pro Thr Phe Asn
 25 30 35

atc aac aac ggc ttc aac gat gct gat gga tcc acc atc cag cca gtt 740
 Ile Asn Asn Gly Phe Asn Asp Ala Asp Gly Ser Thr Ile Gln Pro Val
 40 45 50

gag cca gtt aac cac acc gag gaa acc ctc cgc gac ctg act 782
 Glu Pro Val Asn His Thr Glu Glu Thr Leu Arg Asp Leu Thr
 55 60 65

<210> 5
 <211> 68
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 5
 Met Phe Asn Asn Arg Ile Arg Thr Ala Ala Leu Ala Gly Ala Ile Ala
 1 5 10 15
 Ile Ser Thr Ala Ala Ser Gly Val Ala Ile Pro Ala Phe Ala Gln Glu
 20 25 30
 Thr Asn Pro Thr Phe Asn Ile Asn Asn Gly Phe Asn Asp Ala Asp Gly
 35 40 45
 Ser Thr Ile Gln Pro Val Glu Pro Val Asn His Thr Glu Glu Thr Leu
 50 55 60
 Arg Asp Leu Thr
 65

<210> 6
 <211> 1809
 <212> DNA
 <213> Streptoverticillium mobaraense

<220>
 <221> CDS
 <222> (578)..(1798)

<400> 6
 gtcgacgcgg gcccggaggg ggtgcggcgg cgcccttcgg ctgtgtggac gaagcgtcgg 60
 gtcggagggg cggccggata tcgtccttgg ggcgggggtgg ccggaaattgc cgccatggtg 120
 ttgccgggaa atcgacccga agacatgatc acttctcgta tccacccgat cacgtatccg 180
 ggagtcgaga agtgttacgc cgtgcccctg tccgcgtcct caccctgtc gccgtgacag 240
 cgacccgcgt tcttccactc gcacggacgg ccccacagga ccttcggcc cgggctcgcc 300
 ccgcccgcctc ggtgacggcc tccgaataac gcggccgccc gggcctcgcc cgggttgaccg 360
 atccgggtca cgccgcggc cgggcggggcg gccacgtccg gtctcgcccc gcccacatc 420
 ggctgcgact gccttcgctc gcacttcttc ccgcctcccg gccgcgttt tccggcggcc 480
 aagggtcgccg gacgcgtacc gaatccccct tcatcgac gtgcttccgc acggccgcgt 540
 tcaacgatgt tccacgacaa aggagttgca ggtttcc atg cgc ata cgc cgg aga 595
 Met Arg Ile Arg Arg Arg
 1 5

gct ctc gtc ttc gcc act atg agt gct gtg tta tgc acc gcc gga ttc 643
 Ala Leu Val Phe Ala Thr Met Ser Ala Val Leu Cys Thr Ala Gly Phe
 10 15 20

atg ccg tcg gcc ggc gag gcc gac aat ggc gct ggg gaa gag 691
 Met Pro Ser Ala Gly Glu Ala Ala Asp Asn Gly Ala Gly Glu Glu
 25 30 35

acg aag tcc tac gcc gaa acc tac cgc ctc acg gcg gat gac gtc gcg	739		
Thr Lys Ser Tyr Ala Glu Thr Tyr Arg Leu Thr Ala Asp Asp Val Ala			
40	45	50	
aac atc aac gcg ctc aac gaa agc gct ccg gcc gct tcg acg gcc ggc	787		
Asn Ile Asn Ala Leu Asn Glu Ser Ala Pro Ala Ala Ser Ser Ala Gly			
55	60	65	70
ccg tcg ttc cgg gcc ccc gac tcc gac gac agg gtc acc cct ccc gcc	835		
Pro Ser Phe Arg Ala Pro Asp Ser Asp Asp Arg Val Thr Pro Pro Ala			
75	80	85	
gag ccg ctc gac agg atg ccc gac ccg tac cgt ccc tcg tac ggc agg	883		
Glu Pro Leu Asp Arg Met Pro Asp Pro Tyr Arg Pro Ser Tyr Gly Arg			
90	95	100	
gcc gag acg gtc gtc aac aac tac ata cgc aag tgg cag cag gtc tac	931		
Ala Glu Thr Val Val Asn Asn Tyr Ile Arg Lys Trp Gln Gln Val Tyr			
105	110	115	
agc cac cgc gac ggc agg aag cag cag atg acc gag gag cag cgg gag	979		
Ser His Arg Asp Gly Arg Lys Gln Gln Met Thr Glu Glu Gln Arg Glu			
120	125	130	
tgg ctg tcc tac ggc tgc gtc ggt gtc acc tgg gtc aat tcg ggt cag	1027		
Trp Leu Ser Tyr Gly Cys Val Gly Val Thr Trp Val Asn Ser Gly Gln			
135	140	145	150
tac ccg acg aac aga ctg gcc ttc gcg tcc ttc gac gag gac agg ttc	1075		
Tyr Pro Thr Asn Arg Leu Ala Phe Ala Ser Phe Asp Glu Asp Arg Phe			
155	160	165	
aag aac gag ctg aag aac ggc agg ccc cgg tcc ggc gag acg cgg gcg	1123		
Lys Asn Glu Leu Lys Asn Gly Arg Pro Arg Ser Gly Glu Thr Arg Ala			
170	175	180	
gag ttc gag ggc cgc gtc gcg aag gag agc ttc gac gag gag aag ggc	1171		
Glu Phe Glu Gly Arg Val Ala Lys Glu Ser Phe Asp Glu Glu Lys Gly			
185	190	195	
ttc cag ccg cgc cgt gag gtg gcg tcc gtc atg aac agg gcc ctg gag	1219		
Phe Gln Arg Ala Arg Glu Val Ala Ser Val Met Asn Arg Ala Leu Glu			
200	205	210	
aac gcc cac gac gag agc gct tac ctc gac aac ctc aag aag gaa ctg	1267		
Asn Ala His Asp Glu Ser Ala Tyr Leu Asp Asn Leu Lys Lys Glu Leu			
215	220	225	230
gcg aac ggc aac gac gcc ctg cgc aac gag gac gcc cgt tcc ccg ttc	1315		
Ala Asn Gly Asn Asp Ala Leu Arg Asn Glu Asp Ala Arg Ser Pro Phe			
235	240	245	
tac tcg gcg ctg cgg aac acg ccg tcc ttc aag gag cgg aac gga ggc	1363		
Tyr Ser Ala Leu Arg Asn Thr Pro Ser Phe Lys Glu Arg Asn Gly Gly			
250	255	260	

aat cac gac ccg tcc agg atg aag gcc gtc atc tac tcg aag cac ttc Asn His Asp Pro Ser Arg Met Lys Ala Val Ile Tyr Ser Lys His Phe 265 270 275	1411
tgg agc ggc cag gac ccg tcg agt tcg gcc gac aag agg aag tac ggc Trp Ser Gly Gln Asp Arg Ser Ser Ser Ala Asp Lys Arg Lys Tyr Gly 280 285 290	1459
gac ccg gac gcc ttc cgc ccc gcc ccg ggc acc ggc ctg gtc gac atg Asp Pro Asp Ala Phe Arg Pro Ala Pro Gly Thr Gly Leu Val Asp Met 295 300 305 310	1507
tcg agg gac agg aac att ccg cgc agc ccc acc agc ccc ggt gag gga Ser Arg Asp Arg Asn Ile Pro Arg Ser Pro Thr Ser Pro Gly Glu Gly 315 320 325	1555
ttc gtc aat ttc gac tac ggc tgg ttc ggc gcc cag acg gaa gcg gac Phe Val Asn Phe Asp Tyr Gly Trp Phe Gly Ala Gln Thr Glu Ala Asp 330 335 340	1603
gcc gac aag acc gtc tgg acc cac gga aat cac tat cac gcg ccc aat Ala Asp Lys Thr Val Trp Thr His Gly Asn His Tyr His Ala Pro Asn 345 350 355	1651
ggc agc ctg ggt gcc atg cat gtc tac gag agc aag ttc cgc aac tgg Gly Ser Leu Gly Ala Met His Val Tyr Glu Ser Lys Phe Arg Asn Trp 360 365 370	1699
tcc gag ggt tac tcg gac ttc gac cgc gga gcc tat gtg atc acc ttc Ser Glu Gly Tyr Ser Asp Phe Asp Arg Gly Ala Tyr Val Ile Thr Phe 375 380 385 390	1747
atc ccc aag agc tgg aac acc gcc ccc gac aag gta aag cag ggc tgg Ile Pro Lys Ser Trp Asn Thr Ala Pro Asp Lys Val Lys Gln Gly Trp 395 400 405	1795
ccg tcatgtgagc g Pro	1809

<210> 7
 <211> 407
 <212> PRT
 <213> Streptoverticillium mobaraense

<400> 7 Met Arg Ile Arg Arg Ala Leu Val Phe Ala Thr Met Ser Ala Val 1 5 10 15
Leu Cys Thr Ala Gly Phe Met Pro Ser Ala Gly Glu Ala Ala Ala Asp 20 25 30
Asn Gly Ala Gly Glu Glu Thr Lys Ser Tyr Ala Glu Thr Tyr Arg Leu 35 40 45
Thr Ala Asp Asp Val Ala Asn Ile Asn Ala Leu Asn Glu Ser Ala Pro 50 55 60

Ala Ala Ser Ser Ala Gly Pro Ser Phe Arg Ala Pro Asp Ser Asp Asp
 65 70 75 80
 Arg Val Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Asp Pro Tyr
 85 90 95
 Arg Pro Ser Tyr Gly Arg Ala Glu Thr Val Val Asn Asn Tyr Ile Arg
 100 105 110
 Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Arg Lys Gln Gln Met
 115 120 125
 Thr Glu Glu Gln Arg Glu Trp Leu Ser Tyr Gly Cys Val Gly Val Thr
 130 135 140
 Trp Val Asn Ser Gly Gln Tyr Pro Thr Asn Arg Leu Ala Phe Ala Ser
 145 150 155 160
 Phe Asp Glu Asp Arg Phe Lys Asn Glu Leu Lys Asn Gly Arg Pro Arg
 165 170 175
 Ser Gly Glu Thr Arg Ala Glu Phe Glu Gly Arg Val Ala Lys Glu Ser
 180 185 190
 Phe Asp Glu Glu Lys Gly Phe Gln Arg Ala Arg Glu Val Ala Ser Val
 195 200 205
 Met Asn Arg Ala Leu Glu Asn Ala His Asp Glu Ser Ala Tyr Leu Asp
 210 215 220
 Asn Leu Lys Lys Glu Leu Ala Asn Gly Asn Asp Ala Leu Arg Asn Glu
 225 230 235 240
 Asp Ala Arg Ser Pro Phe Tyr Ser Ala Leu Arg Asn Thr Pro Ser Phe
 245 250 255
 Lys Glu Arg Asn Gly Gly Asn His Asp Pro Ser Arg Met Lys Ala Val
 260 265 270
 Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Arg Ser Ser Ser Ala
 275 280 285
 Asp Lys Arg Lys Tyr Gly Asp Pro Asp Ala Phe Arg Pro Ala Pro Gly
 290 295 300
 Thr Gly Leu Val Asp Met Ser Arg Asp Arg Asn Ile' Pro Arg Ser Pro
 305 310 315 320
 Thr Ser Pro Gly Glu Gly Phe Val Asn Phe Asp Tyr Gly Trp Phe Gly
 325 330 335
 Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Val Trp Thr His Gly Asn
 340 345 350
 His Tyr His Ala Pro Asn Gly Ser Leu Gly Ala Met His Val Tyr Glu
 355 360 365

Ser	Lys	Phe	Arg	Asn	Trp	Ser	Glu	Gly	Tyr	Ser	Asp	Phe	Asp	Arg	Gly
370						375				380					
Ala	Tyr	Val	Ile	Thr	Phe	Ile	Pro	Lys	Ser	Trp	Asn	Thr	Ala	Pro	Asp
385					390				395				400		
Lys	Val	Lys	Gln	Gly	Trp	Pro									
						405									

<210>	8
<211>	1079
<212>	PRT
<213>	Streptomyces albogriseolus

<400>	8														
Asn	Gly	Glu	Asn	Ser	Thr	Ala	Ala	Gly	Ser	Ser	Ala	Ser	Ala	Thr	Ala
1				5				10				15			
Leu	Lys	Gly	Lys	His	Arg	Val	Thr	Leu	Ile	Thr	Gly	Asp	Arg	Val	Ala
20						25					30				
Leu	Asp	Ala	Lys	Gly	Arg	Val	Val	Gly	Leu	Glu	Pro	Ala	Glu	Gly	Arg
35						40					45				
Glu	His	Ile	Pro	Val	Gln	Ile	Arg	Arg	Ser	Asp	Gly	His	Thr	Leu	Val
50						55					60				
Val	Pro	Ala	Asp	Ala	Ala	Arg	Leu	Val	Ala	Ser	Gly	Lys	Leu	Asp	Gln
65						70					75			80	
Arg	Leu	Phe	Asp	Val	Thr	Glu	Leu	Asn	Lys	Ala	Ala	Thr	Arg	Thr	Ala
85								90					95		
His	Arg	Gly	Gly	Leu	Lys	Val	Ile	Val	Gly	Tyr	Arg	Gly	Ala	Ala	Lys
100								105					110		
Ala	Ala	Lys	Ala	Asp	Val	Arg	Asp	Ala	Gly	Thr	Val	Arg	Arg	Thr	Leu
115								120					125		
Thr	Ser	Leu	Asn	Ala	Asp	Ala	Val	Gln	Thr	Pro	Gln	Glu	Ala	Gly	Ala
130							135					140			
Glu	Leu	Trp	Glu	Ala	Val	Thr	Asp	Gly	Asp	Arg	Thr	Ala	Ser	Gly	Val
145								150					155		160
Ala	Arg	Val	Trp	Leu	Asp	Gly	Val	Arg	Lys	Ala	Ser	Leu	Asp	Thr	Ser
165									170					175	
Val	Gly	Gln	Ile	Gly	Thr	Pro	Lys	Ala	Trp	Glu	Ala	Gly	Tyr	Asp	Gly
180								185					190		
Lys	Gly	Val	Lys	Ile	Ala	Val	Leu	Asp	Thr	Gly	Val	Asp	Ala	Thr	His
195							200					205			

Pro Asp Leu Lys Gly Gln Val Thr Ala Ser Lys Asn Phe Thr Ser Ala
 210 215 220
 Pro Thr Thr Gly Asp Val Val Gly His Gly Thr His Val Ala Ser Ile
 225 230 235 240
 Ala Ala Gly Thr Gly Ala Gln Ser Lys Gly Thr Tyr Lys Gly Val Ala
 245 250 255
 Pro Gly Ala Lys Ile Leu Asn Gly Lys Val Leu Asp Asp Ala Gly Phe
 260 265 270
 Gly Asp Asp Ser Gly Ile Leu Ala Gly Met Glu Trp Ala Ala Ala Gln
 275 280 285
 Gly Ala Asp Ile Val Asn Met Ser Leu Gly Gly Met Asp Thr Pro Glu
 290 295 300
 Thr Asp Pro Leu Glu Ala Ala Val Asp Lys Leu Ser Ala Glu Lys Gly
 305 310 315 320
 Ile Leu Phe Ala Ile Ala Ala Gly Asn Glu Gly Pro Gln Ser Ile Gly
 325 330 335
 Ser Pro Gly Ser Ala Asp Ser Ala Leu Thr Val Gly Ala Val Asp Asp
 340 345 350
 Lys Asp Lys Leu Ala Asp Phe Ser Ser Thr Gly Pro Arg Leu Gly Asp
 355 360 365
 Gly Ala Val Lys Pro Asp Leu Thr Ala Pro Gly Val Asp Ile Thr Ala
 370 375 380
 Ala Ser Ala Lys Gly Asn Asp Ile Ala Lys Glu Val Gly Glu Lys Pro
 385 390 395 400
 Ala Gly Tyr Met Thr Ile Ser Gly Thr Ser Met Ala Thr Pro His Val
 405 410 415
 Ala Gly Ala Ala Ala Leu Leu Lys Gln Gln His Pro Glu Trp Lys Tyr
 420 425 430
 Ala Glu Leu Lys Gly Ala Leu Thr Ala Ser Thr Lys Asp Gly Lys Tyr
 435 440 445
 Thr Pro Phe Glu Gln Gly Ser Gly Arg Val Gln Val Asp Lys Ala Ile
 450 455 460
 Thr Gln Thr Val Ile Ala Glu Pro Val Ser Leu Ser Phe Gly Val Gln
 465 470 475 480
 Gln Trp Pro His Ala Asp Asp Lys Pro Val Thr Lys Lys Leu Thr Tyr
 485 490 495
 Arg Asn Leu Gly Thr Glu Asp Val Thr Leu Lys Leu Thr Ser Thr Ala
 500 505 510

Thr Gly Pro Lys Gly Lys Ala Ala Pro Ala Gly Phe Phe Thr Leu Gly
 515 520 525
 Ala Ser Thr Leu Thr Val Pro Ala Asn Gly Thr Ala Ser Val Asp Val
 530 535 540
 Thr Ala Asp Thr Arg Leu Gly Gly Ala Val Asp Gly Thr Tyr Ser Ala
 545 550 555 560
 Tyr Val Val Ala Thr Gly Ala Gly Gln Ser Val Arg Thr Ala Ala Ala
 565 570 575
 Val Glu Arg Glu Val Glu Ser Tyr Asn Val Thr Leu Lys Val Leu Asp
 580 585 590
 Arg Ser Gly Lys Ala Thr Ala Asn Tyr Met Ala Tyr Leu Ser Gly Leu
 595 600 605
 Thr Gly Leu Gly Lys Asp Arg Ser Tyr Ala Pro Tyr Glu Ala Asp Gly
 610 615 620
 Ala Val Ser Val Arg Val Pro Lys Gly Gly Tyr Val Leu Asp Ala Ser
 625 630 635 640
 Val Leu Val Gly Ala Asp Pro Glu Thr Trp Arg Gly Ala Asp Trp Leu
 645 650 655
 Ala Gln Pro Lys Leu Asp Val Thr Arg Asn Thr Thr Val Thr Val Asp
 660 665 670
 Ala Arg Lys Ala Lys Pro Val Lys Val Thr Val Pro Gly Lys Ala Ala
 675 680 685
 Lys Ala Gln Phe Ala Ser Ala Asp Tyr Thr Ile Glu Thr Asn Asp Ser
 690 695 700
 Ala Val Ser Tyr Gly Trp Trp Leu Glu Asn Tyr Ser Gly Phe Arg Ser
 705 710 715 720
 Ala His Leu Gly Pro Gln Ile Thr Asn Gly Thr Leu Ser Gln Gln Trp
 725 730 735
 Asn Thr His Phe Ser Asn Gly Ala Lys Ala Gln Tyr Thr Ala Ile Ser
 740 745 750
 Gly Gly Lys Val Lys Lys Leu Ala Thr Gly Tyr Thr Arg Ala Phe Lys
 755 760 765
 Ala Lys Glu Phe Ala Thr Val Gln Val Gly Met Gly Ala Ala Ala Ser
 770 775 780
 Gly Lys Lys Gly Ala Val Thr Ala Phe Gly Trp Leu Pro Gly Ser Ser
 785 790 795 800
 Gly Ala Ser Gly Phe Ser Gln Glu Gln Lys Leu Pro Ser Thr Arg Thr
 805 810 815

Leu Tyr Leu Ser Thr Val Asn Gly Val Thr Trp Asp Leu Asp Phe Glu
 820 825 830
 Gln Leu Gly Gly Val Asp Asn Glu Gly Trp Pro Ile Tyr Asp Ala Val
 835 840 845
 Tyr Thr Ile Gly Val Gly Lys Thr Tyr Lys Gly Gly Lys Thr Tyr Lys
 850 855 860
 Glu Thr Val Asn Thr Ala Val Phe Gly Pro Arg Leu Thr Ser Ser Tyr
 865 870 875 880
 Gly Val Phe Arg Asp Gly Asn Ser Ile Tyr Gly Val Ile Pro Leu Phe
 885 890 895
 Ala Asp Gly Lys Gly His Ala Gly Ser Ser Glu Phe Ser Ser Ala Val
 900 905 910
 Thr Thr Leu Tyr Arg Asn Gly Lys Lys Val Gly Ser Asn Asn Asp Pro
 915 920 925
 Leu Phe Gly Glu Glu Gly Phe Thr Val Pro Ser Gly Asp Ala Ala Tyr
 930 935 940
 Arg Leu Thr Thr Ser Val Lys Arg Ser Ala Lys Val Ala Ala Ala Ser
 945 950 955 960
 Thr Arg Ile Asp Ala Ser Trp Thr Phe Arg Ser Lys Lys Thr Ser Gly
 965 970 975
 Glu Lys Gln Leu Pro Val Ser Ser Ala Arg Phe Ala Ala Val Thr Gly
 980 985 990
 Leu Asp Ser Lys Val Ala Ala Gly Lys Lys Ala Thr Phe Pro Val Val
 995 1000 1005
 Val Glu Gly Ala Ala Gln Gly Lys Asn Leu Lys Ser Leu Ala Val Tyr
 1010 1015 1020
 Val Ser Tyr Asn Gly Gly Lys Thr Trp Lys Lys Thr Thr Val Thr Lys
 1025 1030 1035 1040
 Gly Lys Ile Thr Val Lys Asn Pro Ala Lys Gly Lys Ala Ile Ser Phe
 1045 1050 1055
 Arg Ala Lys Ile Thr Asp Lys Lys Gly Asn Ala Ser Leu Ile Thr Ile
 1060 1065 1070
 His Asn Ala Tyr Tyr Gly Lys
 1075

<210> 9
 <211> 1751
 <212> DNA
 <213> Streptoverticillium moharaense

<220>
<221> CDS
<222> (229)..(1659)

<400> 9
gctccatatga gcatcgacgc cgccagcagc gatcggttcg gtctgaccgt cgacgccgac 60
ggcgagcgcg tgtggctgga cgagcccggt cggcccggtc cgctcgtgcg gccgtgaaag 120
gccccaaaag agcccaagcc gtgtgaactg cgaggacaaa gggtctggcg caacgcatgt 180
caccggat aagttcgccg cgaccttcg gaaccaggg gagggcgc atg cgc aag 237
Met Arg Lys
1
gct ctc aga tcg ctg ctg gcg gcg tcg atg ctc ata gga gcg atc ggc 285
Ala Leu Arg Ser Leu Leu Ala Ala Ser Met Leu Ile Gly Ala Ile Gly
5 10 15
gcc ggc agc gcc acg gcg gag gcg gcg tcg atc acc gcc ccc cag gcc 333
Ala Gly Ser Ala Thr Ala Glu Ala Ala Ser Ile Thr Ala Pro Gln Ala
20 25 30 35
gac atc aag gac cgc atc ctg aag att ccc ggg atg aag ttc gtc gag 381
Asp Ile Lys Asp Arg Ile Leu Lys Ile Pro Gly Met Lys Phe Val Glu
40 45 50
gag aag ccc tac cag ggc tac cgc tac ctc gtg atg acg tac cgg cag 429
Glu Lys Pro Tyr Gln Gly Tyr Arg Tyr Leu Val Met Thr Tyr Arg Gln
55 60 65
ccg gtg gac cac cgc aat ccc ggc aag ggg acc ttc gag cag cgc ttc 477
Pro Val Asp His Arg Asn Pro Gly Lys Gly Thr Phe Glu Gln Arg Phe
70 75 80
acc ctg ctc cac aag gac acc gac cgg ccc acc gtg ttc ttc acg tcc 525
Thr Leu Leu His Lys Asp Thr Asp Arg Pro Thr Val Phe Phe Thr Ser
85 90 95
ggc tac aac gtc tcc acc aac ccc agc cgc agc gag ccc acg cgc atc 573
Gly Tyr Asn Val Ser Thr Asn Pro Ser Arg Ser Glu Pro Thr Arg Ile
100 105 110 115
gtg gac ggc aac cag gtg tcg atg gag tac cgg ttc ttc acg ccc tcc 621
Val Asp Gly Asn Gln Val Ser Met Glu Tyr Arg Phe Phe Thr Pro Ser
120 125 130
cgg ccg cag ccc gcc gac tgg tcc aag ctg gac atc tgg cag gcg gcg 669
Arg Pro Gln Pro Ala Asp Trp Ser Lys Leu Asp Ile Trp Gln Ala Ala
135 140 145
agt gac cag cac cgc ctg tac cag gcg ctg aag ccg gtc tac ggg aag 717
Ser Asp Gln His Arg Leu Tyr Gln Ala Leu Lys Pro Val Tyr Gly Lys
150 155 160
aac tgg ctg gcc acg ggc ggc agc aag ggc ggc atg acg gcc acc tac 765
Asn Trp Leu Ala Thr Gly Ser Lys Gly Gly Met Thr Ala Thr Tyr

165	170	175	
ttc cgc cgc ttc tac ccg aac gac atg aac ggc acg gtc gcc tac gtc Phe Arg Arg Phe Tyr Pro Asn Asp Met Asn Gly Thr Val Ala Tyr Val	185	190	813
180			195
gcg ccc aac gac gtg aac gac aag gaa gac tcg gcg tac gac aag ttc Ala Pro Asn Asp Val Asn Asp Lys Glu Asp Ser Ala Tyr Asp Lys Phe	200	205	861
			210
ttc cag aac gtc ggc gac aag gcg tgc cgc acg cag ctc aac tcg gtg Phe Gln Asn Val Gly Asp Lys Ala Cys Arg Thr Gln Leu Asn Ser Val	215	220	909
			225
cag cgc gag gcg ctc gtc cgc cgc gac gag atc gtc gcc cgc tac gag Gln Arg Glu Ala Leu Val Arg Arg Asp Glu Ile Val Ala Arg Tyr Glu	230	235	957
			240
aag tgg gct aag gag aac ggc aag acg ttc aag gtc gtc ggc agc gcc Lys Trp Ala Lys Glu Asn Gly Lys Thr Phe Lys Val Val Gly Ser Ala	245	250	1005
			255
gac aag gcg tac gag aac gtc gtc ctc gac ctg gtc tgg tcc ttc tgg Asp Lys Ala Tyr Glu Asn Val Val Leu Asp Leu Val Trp Ser Phe Trp	260	265	1053
			270
275			
cag tac cac ctg cag agc gac tgc gcc tcc gtc ccc gcc acc aag gcg Gln Tyr His Leu Gln Ser Asp Cys Ala Ser Val Pro Ala Thr Lys Ala	280	285	1101
			290
tcc acc gac gag ctg tac aag ttc atc gac gac atc tcg ggc ttc gac Ser Thr Asp Glu Leu Tyr Lys Phe Ile Asp Asp Ile Ser Gly Phe Asp	295	300	1149
			305
ggc tac acc gac cag ggc ctg gag cgc ttc acc ccg tac tac tac cag Gly Tyr Thr Asp Gln Gly Leu Glu Arg Phe Thr Pro Tyr Tyr Gln	310	315	1197
			320
gcg ggc acc cag ctc ggc gcc cct acg gtg aag aac ccg cac ctc aag Ala Gly Thr Gln Leu Gly Ala Pro Thr Val Lys Asn Pro His Leu Lys	325	330	1245
			335
ggc gtg ctg cgg tac ccc ggc atc aac cag ccg cgc tcg tac gtc ccc Gly Val Leu Arg Tyr Pro Gly Ile Asn Gln Pro Arg Ser Tyr Val Pro	340	345	1293
			350
355			
cgc gac atc ccg atg acc ttc cgc ccc ggc gcg atg gcg gac gtc gac Arg Asp Ile Pro Met Thr Phe Arg Pro Gly Ala Met Ala Asp Val Asp	360	365	1341
			370
cgc tgg gtg cgc gag gac agc cgg aac atg ctc ttc gtg tac ggg cag Arg Trp Val Arg Glu Asp Ser Arg Asn Met Leu Phe Val Tyr Gly Gln	375	380	1389
			385
aac gac ccg tgg agc ggt gaa ccg ttc cgc ctg ggc aag ggc gcc gcc Asn Asp Pro Trp Ser Gly Glu Pro Phe Arg Leu Gly Lys Gly Ala Ala	390	395	1437
			400

gcc cg ^g cac gac tac cg ^c ttc tac gcc cc ^g ggc gg ^c aac cac gg ^t tcc	1485		
Ala Arg His Asp Tyr Arg Phe Tyr Ala Pro Gly Gly Asn His Gly Ser			
405	410	415	
aac atc gcc cag ttg gtg gcc gac gag cc ^g aag gcc ac ^c gg ^c gag	1533		
Asn Ile Ala Gln Leu Val Ala Asp Glu Arg Ala Lys Ala Thr Ala Glu			
420	425	430	435
gtc ctg aag tgg gcc ggt gtg gc ^g cc ^g cag gg ^c aag gac gag	1581		
Val Leu Lys Trp Ala Gly Val Ala Pro Gln Ala Val Gln Lys Asp Glu			
440	445	450	
aag gcc g ^c aag cc ^g ctc gc ^g cc ^g ttc gac gg ^c aag ctc gac cc ^g gt ^g	1629		
Lys Ala Ala Lys Pro Leu Ala Pro Phe Asp Ala Lys Leu Asp Arg Val			
455	460	465	
aag aac gac aag cag agc gc ^g ctg cgt cc ^g tagggaccca gtgcgttaagg	1679		
Lys Asn Asp Lys Gln Ser Ala Leu Arg Pro			
470	475		
cggcgggcg ^c tcccggcgag gggcgcccg ^c cgtcgcgttc cggaaaggccc cgggtgcccgc	1739		
cgcccggtgct tc	1751		

<210> 10
 <211> 477
 <212> PRT
 <213> Streptoverticillium mobaraense

<400> 10			
Met Arg Lys Ala Leu Arg Ser Leu Leu Ala Ala Ser Met Leu Ile Gly			
1	5	10	15
Ala Ile Gly Ala Gly Ser Ala Thr Ala Glu Ala Ala Ser Ile Thr Ala			
20	25	30	
Pro Gln Ala Asp Ile Lys Asp Arg Ile Leu Lys Ile Pro Gly Met Lys			
35	40	45	
Phe Val Glu Glu Lys Pro Tyr Gln Gly Tyr Arg Tyr Leu Val Met Thr			
50	55	60	
Tyr Arg Gln Pro Val Asp His Arg Asn Pro Gly Lys Gly Thr Phe Glu			
65	70	75	80
Gln Arg Phe Thr Leu Leu His Lys Asp Thr Asp Arg Pro Thr Val Phe			
85	90	95	
Phe Thr Ser Gly Tyr Asn Val Ser Thr Asn Pro Ser Arg Ser Glu Pro			
100	105	110	
Thr Arg Ile Val Asp Gly Asn Gln Val Ser Met Glu Tyr Arg Phe Phe			
115	120	125	
Thr Pro Ser Arg Pro Gln Pro Ala Asp Trp Ser Lys Leu Asp Ile Trp			

130	135	140
Gln Ala Ala Ser Asp Gln His Arg Leu Tyr Gln Ala Leu Lys Pro Val		
145	150	155
160		
Tyr Gly Lys Asn Trp Leu Ala Thr Gly Gly Ser Lys Gly Gly Met Thr		
165	170	175
Ala Thr Tyr Phe Arg Arg Phe Tyr Pro Asn Asp Met Asn Gly Thr Val		
180	185	190
Ala Tyr Val Ala Pro Asn Asp Val Asn Asp Lys Glu Asp Ser Ala Tyr		
195	200	205
Asp Lys Phe Phe Gln Asn Val Gly Asp Lys Ala Cys Arg Thr Gln Leu		
210	215	220
Asn Ser Val Gln Arg Glu Ala Leu Val Arg Arg Asp Glu Ile Val Ala		
225	230	235
240		
Arg Tyr Glu Lys Trp Ala Lys Glu Asn Gly Lys Thr Phe Lys Val Val		
245	250	255
Gly Ser Ala Asp Lys Ala Tyr Glu Asn Val Val Leu Asp Leu Val Trp		
260	265	270
Ser Phe Trp Gln Tyr His Leu Gln Ser Asp Cys Ala Ser Val Pro Ala		
275	280	285
Thr Lys Ala Ser Thr Asp Glu Leu Tyr Lys Phe Ile Asp Asp Ile Ser		
290	295	300
Gly Phe Asp Gly Tyr Thr Asp Gln Gly Leu Glu Arg Phe Thr Pro Tyr		
305	310	315
320		
Tyr Tyr Gln Ala Gly Thr Gln Leu Gly Ala Pro Thr Val Lys Asn Pro		
325	330	335
His Leu Lys Gly Val Leu Arg Tyr Pro Gly Ile Asn Gln Pro Arg Ser		
340	345	350
Tyr Val Pro Arg Asp Ile Pro Met Thr Phe Arg Pro Gly Ala Met Ala		
355	360	365
Asp Val Asp Arg Trp Val Arg Glu Asp Ser Arg Asn Met Leu Phe Val		
370	375	380
Tyr Gly Gln Asn Asp Pro Trp Ser Gly Glu Pro Phe Arg Leu Gly Lys		
385	390	395
400		
Gly Ala Ala Ala Arg His Asp Tyr Arg Phe Tyr Ala Pro Gly Gly Asn		
405	410	415
His Gly Ser Asn Ile Ala Gln Leu Val Ala Asp Glu Arg Ala Lys Ala		
420	425	430
Thr Ala Glu Val Leu Lys Trp Ala Gly Val Ala Pro Gln Ala Val Gln		

435 440 445
Lys Asp Glu Lys Ala Ala Lys Pro Leu Ala Pro Phe Asp Ala Lys Leu
450 455 460
Asp Arg Val Lys Asn Asp Lys Gln Ser Ala Leu Arg Pro
465 470 475

<210> 11
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 11
gactccgacg acagggtcac ccctcccgcc 30

<210> 12
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 12
cgctcacatc acggccagcc ctgctttacc 30

<210> 13
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer for
the promoter region and signal sequence region of
S.mobaraense

<400> 13
gtgaccctgt cgtcgaggatc 20

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer for
the promoter region and signal sequence region of
S.mobaraense

<400> 14	20
ggcatcctgt cgagcggctc	
<210> 15	
<211> 26	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence:PCR primer	
<400> 15	26
aaattcctgt gaatttagctg atttag	
<210> 16	
<211> 44	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence:PCR primer	
<400> 16	44
gagctctccg gcgtatgcgc atagaggcga aggctcccttg aata	
<210> 17	
<211> 30	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence:PCR primer	
<400> 17	30
atgcgcatac gccggagagc tctcgtcttc	
<210> 18	
<211> 47	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> Description of Artificial Sequence:PCR primer	
<400> 18	47
ggggtgaccc tgtcgtcgga gtcgttgaag ccgttgttga tgttgaa	
<210> 19	
<211> 51	
<212> DNA	
<213> Artificial Sequence	

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 19
cttcgtctct tcccccgcbc cattgtcagc gaatgctggg atagcaacgc c 51

<210> 20
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 20
cttcgtctct tcccccgcbc cattgtcctg agcgaatgct gggatagcta c 51

<210> 21
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 21
cttcgtctct tcccccgcbc cattgtcggt gaagccgttg ttgatgttga a 51

<210> 22
<211> 51
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 22
cttcgtctct tcccccgcbc cattgtcagt caggtcgccg agggtttcct c 51

<210> 23
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 23
gacaatggcg cggggagaaga gacgaagtcc 30

<210> 24

<211> 25		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence:PCR primer		
<400> 24		25
gccccagaagc ccaaaattga gattt		
<210> 25		
<211> 52		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence:PCR primer		
<400> 25		52
cttcgtctct tcccccgcgc cattgtctgc cgttgccaca ggtgcggcca gc		
<210> 26		
<211> 52		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence:PCR primer		
<400> 26		52
cgcagccagc gatttcatgc gtttcataga ggcgaaggct ctttgaatag gt		
<210> 27		
<211> 30		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence:PCR primer		
<400> 27		30
atgaaacgca tgaaatcgct ggctgcggcg		
<210> 28		
<211> 25		
<212> DNA		
<213> Artificial Sequence		
<220>		
<223> Description of Artificial Sequence:PCR primer		
<400> 28		25
ggatccggag cttatcgact gcacg		

<210> 29
 <211> 52
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:PCR primer

<400> 29
 cgcagccagc gattcatgc gtttcataat tctgtttcct gtgtgaaatt gt 52

<210> 30
 <211> 1461
 <212> DNA
 <213> Streptoverticillium cinnamoneum

<220>
 <221> CDS
 <222> (151)..(1398)

<400> 30
 cgccggcagc ctccttgcc gccggcgcaag cgacgcagga cggcgccggcc aaggccctga 60
 gccggcagctc gtcgcaaacc ctcctatcgc gtcgtgtct cacatgcctt cgtttacga 120
 ggcttcacca caagggagtt attgatttcc atg cac aaa cgt cgg aga ctt ctc 174
 Met His Lys Arg Arg Arg Leu Leu
 1 5

gcc ttc gcc act gtg ggt gcg gtc ata tgc acc gca gga ttc aca cct 222
 Ala Phe Ala Thr Val Gly Ala Val Ile Cys Thr Ala Gly Phe Thr Pro
 10 15 20

tcg gtc agc cag gcc gcc agc agt ggc gat ggg gaa gag aag ggg tcc 270
 Ser Val Ser Gln Ala Ala Ser Ser Gly Asp Gly Glu Lys Gly Ser
 25 30 35 40

tac gcc gaa acg cac ggc ctg acg gcg gat gac gtc gag agc atc aac 318
 Tyr Ala Glu Thr His Gly Leu Thr Ala Asp Asp Val Glu Ser Ile Asn
 45 50 55

gca ctg aac gaa aga gct ctg act ctg ggc caa cct ggc aag cct ccg 366
 Ala Leu Asn Glu Arg Ala Leu Thr Leu Gly Gln Pro Gly Lys Pro Pro
 60 65 70

aag gaa tta cct ccg agc gcc agc gcg ccc tcc cgg gcc ccc tcc gat 414
 Lys Glu Leu Pro Pro Ser Ala Ser Ala Pro Ser Arg Ala Pro Ser Asp
 75 80 85

gac cgg gaa act cct ccc gcc gag ccg ctc gac agg atg cct gag gcg 462
 Asp Arg Glu Thr Pro Pro Ala Glu Pro Leu Asp Arg Met Pro Glu Ala
 90 95 100

tac cgg gcc tac gga ggc agg gcc act acg gtc aac aac tac ata 510

Tyr Arg Ala Tyr Gly Gly Arg Ala Thr Thr Val Val Asn Asn Tyr Ile			
105	110	115	120
cgc aag tgg cag cag gtc tac agt cac cgc gac gga aag aaa cag caa			558
Arg Lys Trp Gln Gln Val Tyr Ser His Arg Asp Gly Lys Lys Gln Gln			
125	130	135	
atg acc gaa gag cag cga gaa aag ctg tcc tac ggt tgc gtt ggc gtc			606
Met Thr Glu Glu Gln Arg Glu Lys Leu Ser Tyr Gly Cys Val Gly Val			
140	145	150	
acc tgg gtc aac tcg ggc ccc tac ccg acg aac aga ttg gcg ttc gcg			654
Thr Trp Val Asn Ser Gly Pro Tyr Pro Thr Asn Arg Leu Ala Phe Ala			
155	160	165	
tcc ttc gac gag aac aag tac aag aac gac ctg aag aac acc agc ccc			702
Ser Phe Asp Glu Asn Lys Tyr Lys Asn Asp Leu Lys Asn Thr Ser Pro			
170	175	180	
cga ccc gat gaa acg cgg gcg gag ttc gag ggt cgc atc gcc aag ggc			750
Arg Pro Asp Glu Thr Arg Ala Glu Phe Glu Gly Arg Ile Ala Lys Gly			
185	190	195	200
agt ttc gac gag ggg aag ggt ttc aag cgg gcg cgt gat gtg gcg tcc			798
Ser Phe Asp Glu Gly Lys Gly Phe Lys Arg Ala Arg Asp Val Ala Ser			
205	210	215	
gtc atg aac aag gcc ctg gaa aat gcc cac gac gag ggg act tac atc			846
Val Met Asn Lys Ala Leu Glu Asn Ala His Asp Glu Gly Thr Tyr Ile			
220	225	230	
aac aac ctc aag acg gag ctc acg aac aac aat gac gct ctg ctc cgc			894
Asn Asn Leu Lys Thr Glu Leu Thr Asn Asn Asp Ala Leu Leu Arg			
235	240	245	
gag gac agc cgc tcg aac ttc tac tcg gcg ctg agg aac aca ccg tcc			942
Glu Asp Ser Arg Ser Asn Phe Tyr Ser Ala Leu Arg Asn Thr Pro Ser			
250	255	260	
ttc aag gaa agg gac ggc ggc aac tac gac ccg tcc aag atg aag gcg			990
Phe Lys Glu Arg Asp Gly Gly Asn Tyr Asp Pro Ser Lys Met Lys Ala			
265	270	275	280
gtg atc tac tcg aag cac ttc tgg agc ggg cag gac cag cgg ggc tcc			1038
Val Ile Tyr Ser Lys His Phe Trp Ser Gly Gln Asp Gln Arg Gly Ser			
285	290	295	
tcc gac aag agg aag tac ggc gac ccg gaa gcc ttc cgc ccc gac cag			1086
Ser Asp Lys Arg Lys Tyr Gly Asp Pro Glu Ala Phe Arg Pro Asp Gln			
300	305	310	
ggt acc ggc ctg gtc gac atg tcg aag gac aga agc att ccg cgc agt			1134
Gly Thr Gly Leu Val Asp Met Ser Lys Asp Arg Ser Ile Pro Arg Ser			
315	320	325	
ccg gcc aag ccc ggc gaa ggt tgg gtc aat ttc gac tac ggt tgg ttc			1182
Pro Ala Lys Pro Gly Glu Gly Trp Val Asn Phe Asp Tyr Gly Trp Phe			

330	335	340	
ggg gct caa aca gaa gcg gat gcc gac aaa acc aca tgg acc cac ggc			1230
Gly Ala Gln Thr Glu Ala Asp Ala Asp Lys Thr Thr Trp Thr His Gly			
345	350	355	360
gac cac tac cac gcg ccc aat agc gac ctg ggc ccc atg cac gta cac			1278
Asp His Tyr His Ala Pro Asn Ser Asp Leu Gly Pro Met His Val His			
365	370	375	
gag agc aag ttc cg ^g aag tgg tct gcc ggg tac gcg gac ttc gac cgc			1326
Glu Ser Lys Phe Arg Lys Trp Ser Ala Gly Tyr Ala Asp Phe Asp Arg			
380	385	390	
gga gcc tac gtg atc acg ttc ata ccc aag agc tgg aac acc gcc ccc			1374
Gly Ala Tyr Val Ile Thr Phe Ile Pro Lys Ser Trp Asn Thr Ala Pro			
395	400	405	
gcc aag gtg gag caa ggc tgg ccg tgacaggctg gtactacgac ctctgctgat			1428
Ala Lys Val Glu Gln Gly Trp Pro			
410	415		
ttctgcccgg tcagtcacg cctctcgacg cga			1461
<210> 31			
<211> 416			
<212> PRT			
<213> Streptoverticillium cinnamoneum			
<400> 31			
Met His Lys Arg Arg Arg Leu Leu Ala Phe Ala Thr Val Gly Ala Val			
1	5	10	15
Ile Cys Thr Ala Gly Phe Thr Pro Ser Val Ser Gln Ala Ala Ser Ser			
20	25	30	
Gly Asp Gly Glu Glu Lys Gly Ser Tyr Ala Glu Thr His Gly Leu Thr			
35	40	45	
Ala Asp Asp Val Glu Ser Ile Asn Ala Leu Asn Glu Arg Ala Leu Thr			
50	55	60	
Leu Gly Gln Pro Gly Lys Pro Pro Lys Glu Leu Pro Pro Ser Ala Ser			
65	70	75	80
Ala Pro Ser Arg Ala Pro Ser Asp Asp Arg Glu Thr Pro Pro Ala Glu			
85	90	95	
Pro Leu Asp Arg Met Pro Glu Ala Tyr Arg Ala Tyr Gly Arg Ala			
100	105	110	
Thr Thr Val Val Asn Asn Tyr Ile Arg Lys Trp Gln Gln Val Tyr Ser			
115	120	125	
His Arg Asp Gly Lys Lys Gln Gln Met Thr Glu Glu Gln Arg Glu Lys			
130	135	140	

Leu Ser Tyr Gly Cys Val Gly Val Thr Trp Val Asn Ser Gly Pro Tyr
 145 150 155 160
 Pro Thr Asn Arg Leu Ala Phe Ala Ser Phe Asp Glu Asn Lys Tyr Lys
 165 170 175
 Asn Asp Leu Lys Asn Thr Ser Pro Arg Pro Asp Glu Thr Arg Ala Glu
 180 185 190
 Phe Glu Gly Arg Ile Ala Lys Gly Ser Phe Asp Glu Gly Lys Gly Phe
 195 200 205
 Lys Arg Ala Arg Asp Val Ala Ser Val Met Asn Lys Ala Leu Glu Asn
 210 215 220
 Ala His Asp Glu Gly Thr Tyr Ile Asn Asn Leu Lys Thr Glu Leu Thr
 225 230 235 240
 Asn Asn Asn Asp Ala Leu Leu Arg Glu Asp Ser Arg Ser Asn Phe Tyr
 245 250 255
 Ser Ala Leu Arg Asn Thr Pro Ser Phe Lys Glu Arg Asp Gly Gly Asn
 260 265 270
 Tyr Asp Pro Ser Lys Met Lys Ala Val Ile Tyr Ser Lys His Phe Trp
 275 280 285
 Ser Gly Gln Asp Gln Arg Gly Ser Ser Asp Lys Arg Lys Tyr Gly Asp
 290 295 300
 Pro Glu Ala Phe Arg Pro Asp Gln Gly Thr Gly Leu Val Asp Met Ser
 305 310 315 320
 Lys Asp Arg Ser Ile Pro Arg Ser Pro Ala Lys Pro Gly Glu Gly Trp
 325 330 335
 Val Asn Phe Asp Tyr Gly Trp Phe Gly Ala Gln Thr Glu Ala Asp Ala
 340 345 350
 Asp Lys Thr Thr Trp Thr His Gly Asp His Tyr His Ala Pro Asn Ser
 355 360 365
 Asp Leu Gly Pro Met His Val His Glu Ser Lys Phe Arg Lys Trp Ser
 370 375 380
 Ala Gly Tyr Ala Asp Phe Asp Arg Gly Ala Tyr Val Ile Thr Phe Ile
 385 390 395 400
 Pro Lys Ser Trp Asn Thr Ala Pro Ala Lys Val Glu Gln Gly Trp Pro
 405 410 415

<210> 32
 <211> 21
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 32
ggcgatgggg aagagaaggg g 21

<210> 33

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 33
ggcggatcct cgcgtcgaga ggcgtggact ga 32

<210> 34

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 34
tacgaattcg agctcggtac c 21

<210> 35

<211> 43

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 35
cccccattcttgc ctgccgttgc cacaggtgcg gcc 43

<210> 36

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 36
aacggggaga acagcacggc cgccgg 26

```

<210> 37
<211> 29
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 37
ggcgaattct ccggcgggcc gtcaccggt 29

<210> 38
<211> 30
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer for
      fused prepro-serineprotease construction

<400> 38
ggcaagctta aattcctgtg aattagctga 30

<210> 39
<211> 44
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer for
      fused prepro-serineprotease gene construction

<400> 39
cggccgtgt gttctccccc tttgccgttg ccacaggtgc ggcc 44

<210> 40
<211> 20
<212> PRT
<213> Streptoverticillium moharaence

<400> 40
Gln Ala Asp Ile Lys Asp Arg Ile Leu Lys Ile Pro Gly Met Lys Phe
  1           5           10          15

Val Glu Glu Lys
  20

<210> 41
<211> 11
<212> PRT
<213> Artificial Sequence

<220>

```

<223> Description of Artificial Sequence:probe for svPEP

<400> 41
Lys Ile Pro Gly Met Lys Phe Val Glu Glu Lys
1 5 10

<210> 42
<211> 33
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:probe for svPEP

<400> 42
aagatccccc ggtatgaagtt cgtcgaggag aag 33

<210> 43
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 43
gaggcgccgt cgatcaccgc ccc 23

<210> 44
<211> 32
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 44
gccaagcttg aagcacccggc ggcggcaccc gg 32

<210> 45
<211> 46
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 45
ggggcggtga tcgacgcccgc ctctgccgtt gccacaggtg cggcca 46

<210> 46
<211> 37

```

<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 46
gctcggtacc caaattcctg tgaattagct gatttag 37

<210> 47
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 47
gttgaagccg ttgttgatgt tgaa 24

<210> 48
<211> 42
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 48
aacatcaaca acggcttcaa caattccgat tctgagtgcc ct 42

<210> 49
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 49
cgcccacgat gcgtccggcg 20

<210> 50
<211> 43
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 50
agggcactca gaatcggaat ttgccgttgc cacaggtgcg gcc 43

```

```

<210> 51
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 51
aattccgatt ctgagtgccc t 21

<210> 52
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 52
gaattcggc tcggtaacca 20

<210> 53
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 53
agcgatttca tgcgttcat agaggcgaag gtccttgaa 40

<210> 54
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 54
atgaaacgcg taaaatcgct ggc 23

<210> 55
<211> 53
<212> PRT
<213> Homo sapiens

<400> 55
Asn Ser Asp Ser Glu Cys Pro Leu Ser His Asp Gly Tyr Cys Leu His
1 5 10 15

```

Asp Gly Val Cys Met Tyr Ile Glu Ala Leu Asp Lys Tyr Ala Cys Asn
20 25 30

Cys Val Val Gly Tyr Ile Gly Glu Arg Cys Gln Tyr Arg Asp Leu Lys
35 40 45

Trp Trp Glu Leu Arg
50

<210> 56
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 56
actgggaggc tatctccatt 20

<210> 57
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 57
atcgatctga tcacgttaca 20

<210> 58
<211> 40
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 58
tgtaacgtga tcagatcgat tcactggtcg acaccgttga 40

<210> 59
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:PCR primer

<400> 59
acggaagcta cttcgaggt 20

<210> 60
<211> 4
<212> PRT
<213> *Streptoverticillium moharaense*

<400> 60
Phe Arg Ala Pro
1

1